



SEQUENCE LISTING

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SEP 27 2001
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(1) GENERAL INFORMATION:

(i) APPLICANT: Chandrasekharappa, Settara C.
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Manickam, Pachiappan
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Emmert-Buck, Michael R.
Debelenko, Larisa V.
Lubensky, Irina A.
Liotta, Lance A.
Agarwal, Sunita K.
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(ii) TITLE OF INVENTION: MEN1, the Gene Associated With Multiple
Endocrine Neoplasia Type 1, Menin Polypeptides, and Uses
Thereof

(iii) NUMBER OF SEQUENCES: 28

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: San Francisco
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/380,337
(B) FILING DATE: 06-MAR-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/040,269
(B) FILING DATE: 05-MAR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/US98/04258
(B) FILING DATE: 04-MAR-1998

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 44,879
(C) REFERENCE/DOCKET NUMBER: 015280-315100US

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 111..1940
- (D) OTHER INFORMATION: /product= "human menin"

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1..87

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 88..555

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 556..764

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 765..893

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 894..934

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 935..1022

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1023..1159

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1160..1295

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1296..1460

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1461..2764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTGTCCGGA GCCGCGGACC TAGAGATCCC AGAAGCCACA GCGCAGCGGC CCGGCCCGCC

TAC ATG CGC TGT GAC CGC AAG ATG GAG GTG GCG TTC ATG GTG TGT GCC	836
Tyr Met Arg Cys Asp Arg Lys Met Glu Val Ala Phe Met Val Cys Ala	
230 235 240	
ATC AAC CCT TCC ATT GAC CTG CAC ACC GAC TCG CTG GAG CTT CTG CAG	884
Ile Asn Pro Ser Ile Asp Leu His Thr Asp Ser Leu Glu Leu Leu Gln	
245 250 255	
CTG CAG CAG AAG CTG CTC TGG CTG CTC TAT GAC CTG GGA CAT CTG GAA	932
Leu Gln Gln Lys Leu Leu Trp Leu Leu Tyr Asp Leu Gly His Leu Glu	
260 265 270	
AGG TAC CCC ATG GCC TTA GGG AAC CTG GCA GAT CTA GAG GAG CTG GAG	980
Arg Tyr Pro Met Ala Leu Gly Asn Leu Ala Asp Leu Glu Glu Leu Glu	
275 280 285 290	
CCC ACC CCT GGC CGG CCA GAC CCA CTC ACC CTC TAC CAC AAG GGC ATT	1028
Pro Thr Pro Gly Arg Pro Asp Pro Leu Thr Leu Tyr His Lys Gly Ile	
295 300 305	
GCC TCA GCC AAG ACC TAC TAT CGG GAT GAA CAC ATC TAC CCC TAC ATG	1076
Ala Ser Ala Lys Thr Tyr Tyr Arg Asp Glu His Ile Tyr Pro Tyr Met	
310 315 320	
TAC CTG GCT GGC TAC CAC TGT CGC AAC CGC AAT GTG CGG GAA GCC CTG	1124
Tyr Leu Ala Gly Tyr His Cys Arg Asn Arg Asn Val Arg Glu Ala Leu	
325 330 335	
CAG GCC TGG GCG GAC ACG GCC ACT GTC ATC CAG GAC TAC AAC TAC TGC	1172
Gln Ala Trp Ala Asp Thr Ala Thr Val Ile Gln Asp Tyr Asn Tyr Cys	
340 345 350	
CGG GAA GAC GAG GAG ATC TAC AAG GAG TTC TTT GAA GTA GCC AAT GAT	1220
Arg Glu Asp Glu Glu Ile Tyr Lys Glu Phe Phe Glu Val Ala Asn Asp	
355 360 365 370	
GTC ATC CCC AAC CTG CTG AAG GAG GCA GCC AGC TTG CTG GAG GCG GGC	1268
Val Ile Pro Asn Leu Leu Lys Glu Ala Ala Ser Leu Leu Glu Ala Gly	
375 380 385	
GAG GAG CGG CCG GGG GAG CAA AGC CAG GGC ACC CAG AGC CAA GGT TCC	1316
Glu Glu Arg Pro Gly Glu Gln Ser Gln Gly Thr Gln Ser Gln Gly Ser	
390 395 400	
GCC CTC CAG GAC CCT GAG TGC TTC GCC CAC CTG CTG CGA TTC TAC GAC	1364
Ala Leu Gln Asp Pro Glu Cys Phe Ala His Leu Leu Arg Phe Tyr Asp	
405 410 415	
GGC ATC TGC AAA TGG GAG GAG GGC AGT CCC ACG CCT GTG CTG CAC GTG	1412
Gly Ile Cys Lys Trp Glu Glu Gly Ser Pro Thr Pro Val Leu His Val	
420 425 430	
GGC TGG GCC ACC TTT CTT GTG CAG TCC CTA GGC CGT TTT GAG GGA CAG	1460
Gly Trp Ala Thr Phe Leu Val Gln Ser Leu Gly Arg Phe Glu Gly Gln	
435 440 445 450	
GTG CGG CAG AAG GTG CGC ATA GTG AGC CGA GAG GCC GAG GCG GCC GAG	1508
Val Arg Gln Lys Val Arg Ile Val Ser Arg Glu Ala Glu Ala Ala Glu	
455 460 465	

GCC GAG GAG CCG TGG GGC GAG GAA GCC CGG GAA GGC CGG CGG CGG GGC Ala Glu Glu Pro Trp Gly Glu Glu Ala Arg Glu Gly Arg Arg Arg Gly 470 475 480	1556
CCA CGG CGG GAG TCC AAG CCA GAG GAG CCC CCG CCG CCC AAG AAG CCA Pro Arg Arg Glu Ser Lys Pro Glu Glu Pro Pro Pro Pro Lys Lys Pro 485 490 495	1604
GCA CTG GAC AAG GGC CTG GGC ACC GGC CAG GGT GCA GTG TCA GGA CCC Ala Leu Asp Lys Gly Leu Gly Thr Gly Gln Gly Ala Val Ser Gly Pro 500 505 510	1652
CCC CGG AAG CCT CCT GGG ACT GTC GCT GGC ACA GCC CGA GGC CCT GAA Pro Arg Lys Pro Pro Gly Thr Val Ala Gly Thr Ala Arg Gly Pro Glu 515 520 525 530	1700
GGT GGC AGC ACG GCT CAG GTG CCA GCA CCC GCA GCA TCA CCA CCG CCG Gly Gly Ser Thr Ala Gln Val Pro Ala Pro Ala Ala Ser Pro Pro Pro 535 540 545	1748
GAG GGT CCA GTG CTC ACT TTC CAG AGT GAG AAG ATG AAG GGC ATG AAG Glu Gly Pro Val Leu Thr Phe Gln Ser Glu Lys Met Lys Gly Met Lys 550 555 560	1796
GAG CTG CTG GTG GCC ACC AAG ATC AAC TCG AGC GCC ATC AAG CTG CAA Glu Leu Leu Val Ala Thr Lys Ile Asn Ser Ser Ala Ile Lys Leu Gln 565 570 575	1844
CTC ACG GCA CAG TCG CAA GTG CAG ATG AAG AAG CAG AAA GTG TCC ACC Leu Thr Ala Gln Ser Gln Val Gln Met Lys Lys Gln Lys Val Ser Thr 580 585 590	1892
CCT AGT GAC TAC ACT CTG TCT TTC CTC AAG CGG CAG CGC AAA GGC CTC Pro Ser Asp Tyr Thr Leu Ser Phe Leu Lys Arg Gln Arg Lys Gly Leu 595 600 605 610	1940
TGAACTACTG GGGACTTCGG ACCGCTTG TG GGGACCCAGG CTCCGCCTTA GTCCCCAAC	2000
TCTGAGCCCA TGTTCTGCCC CCAGCCCAAA GGGGACAGGC CTCACCTCTA CCCAAACCCT	2060
AGGTTCCCGG TCCCAGGTAC AGTCTGTATC AAACCCACGA TTTTCTCCAG CTCAGAACCC	2120
AGGGCTCTGC CCCAGTCGTT AGAATATAGG TCTCTTCTCC CAGAATCCCA GCCGGCCAAT	2180
GGAAACCTCA CGCTGGGTCC TAATTACCAG TCTTTAAAGG CCCAGCCCCT AGAAACCCAA	2240
GCTCCTCCTC GGAACCGCTC ACCTAGAGCC AGACCAACGT TACTCAGGGC TCCTCCCAGC	2300
TTGTAGGAGC TGAGGTTTCA CCCTTAACCC AAGGGAGCAC AGGTCCCACC TCCAGCCCGG	2360
GGAGCCTAGG ACCACTCAGC CCCTAGGAGT ATATTTCCGC ACTTCAGAAT TCCATATCTT	2420
GCGAATCCAA GCTCCCTGCC CCAAATAACT TCAGTCCTGC TTCCAGAATT TGGAATCCT	2480
AGTTTCCTCT CCTTCGTATC CCGAGTCTGG GACACAAAAC TCCGCCCCCA GCCTATGAGC	2540
ATCCTGAGCC CCGCCCTCTT CTGACGAAA CTGGCCCCGG ATCAGAGCAG GACCTCCCTT	2600
CCGACCCCTCT GGGAACCTCC CAGAGGTCCA GCCCATCTCG GAGCATCCCG GAGGAAATCT	2660
GCAGAGGGGT TAGGAGTGGG TGACAAGAGC CTGATCTCTT CCTGTTTGT ACATAGATTT	2720

ATTTTTCAGT TCCAAGAAAG ATGAATACAT TTTGTTAAAA AAAAAAAAAA AA

2772

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Leu Lys Ala Ala Gln Lys Thr Leu Phe Pro Leu Arg Ser Ile
1 5 10 15

Asp Asp Val Val Arg Leu Phe Ala Ala Glu Leu Gly Arg Glu Glu Pro
20 25 30

Asp Leu Val Leu Leu Ser Leu Val Leu Gly Phe Val Glu His Phe Leu
35 40 45

Ala Val Asn Arg Val Ile Pro Thr Asn Val Pro Glu Leu Thr Phe Gln
50 55 60

Pro Ser Pro Ala Pro Asp Pro Pro Gly Gly Leu Thr Tyr Phe Pro Val
65 70 75 80

Ala Asp Leu Ser Ile Ile Ala Ala Leu Tyr Ala Arg Phe Thr Ala Gln
85 90 95

Ile Arg Gly Ala Val Asp Leu Ser Leu Tyr Pro Arg Glu Gly Gly Val
100 105 110

Ser Ser Arg Glu Leu Val Lys Lys Val Ser Asp Val Ile Trp Asn Ser
115 120 125

Leu Ser Arg Ser Tyr Phe Lys Asp Arg Ala His Ile Gln Ser Leu Phe
130 135 140

Ser Phe Ile Thr Gly Thr Lys Leu Asp Ser Ser Gly Val Ala Phe Ala
145 150 155 160

Val Val Gly Ala Cys Gln Ala Leu Gly Leu Arg Asp Val His Leu Ala
165 170 175

Leu Ser Glu Asp His Ala Trp Val Val Phe Gly Pro Asn Gly Glu Gln
180 185 190

Thr Ala Glu Val Thr Trp His Gly Lys Gly Asn Glu Asp Arg Arg Gly
195 200 205

Gln Thr Val Asn Ala Gly Val Ala Glu Arg Ser Trp Leu Tyr Leu Lys
210 215 220

Gly Ser Tyr Met Arg Cys Asp Arg Lys Met Glu Val Ala Phe Met Val
225 230 235 240

Cys Ala Ile Asn Pro Ser Ile Asp Leu His Thr Asp Ser Leu Glu Leu
245 250 255

Leu Gln Leu Gln Gln Lys Leu Leu Trp Leu Leu Tyr Asp Leu Gly His
 260 265 270
 Leu Glu Arg Tyr Pro Met Ala Leu Gly Asn Leu Ala Asp Leu Glu Glu
 275 280 285
 Leu Glu Pro Thr Pro Gly Arg Pro Asp Pro Leu Thr Leu Tyr His Lys
 290 295 300
 Gly Ile Ala Ser Ala Lys Thr Tyr Tyr Arg Asp Glu His Ile Tyr Pro
 305 310 315 320
 Tyr Met Tyr Leu Ala Gly Tyr His Cys Arg Asn Arg Asn Val Arg Glu
 325 330 335
 Ala Leu Gln Ala Trp Ala Asp Thr Ala Thr Val Ile Gln Asp Tyr Asn
 340 345 350
 Tyr Cys Arg Glu Asp Glu Glu Ile Tyr Lys Glu Phe Phe Glu Val Ala
 355 360 365
 Asn Asp Val Ile Pro Asn Leu Leu Lys Glu Ala Ala Ser Leu Leu Glu
 370 375 380
 Ala Gly Glu Glu Arg Pro Gly Glu Gln Ser Gln Gly Thr Gln Ser Gln
 385 390 395 400
 Gly Ser Ala Leu Gln Asp Pro Glu Cys Phe Ala His Leu Leu Arg Phe
 405 410 415
 Tyr Asp Gly Ile Cys Lys Trp Glu Glu Gly Ser Pro Thr Pro Val Leu
 420 425 430
 His Val Gly Trp Ala Thr Phe Leu Val Gln Ser Leu Gly Arg Phe Glu
 435 440 445
 Gly Gln Val Arg Gln Lys Val Arg Ile Val Ser Arg Glu Ala Glu Ala
 450 455 460
 Ala Glu Ala Glu Glu Pro Trp Gly Glu Glu Ala Arg Glu Gly Arg Arg
 465 470 475 480
 Arg Gly Pro Arg Arg Glu Ser Lys Pro Glu Glu Pro Pro Pro Pro Lys
 485 490 495
 Lys Pro Ala Leu Asp Lys Gly Leu Gly Thr Gly Gln Gly Ala Val Ser
 500 505 510
 Gly Pro Pro Arg Lys Pro Pro Gly Thr Val Ala Gly Thr Ala Arg Gly
 515 520 525
 Pro Glu Gly Gly Ser Thr Ala Gln Val Pro Ala Pro Ala Ala Ser Pro
 530 535 540
 Pro Pro Glu Gly Pro Val Leu Thr Phe Gln Ser Glu Lys Met Lys Gly
 545 550 555 560
 Met Lys Glu Leu Leu Val Ala Thr Lys Ile Asn Ser Ser Ala Ile Lys
 565 570 575

Leu Gln Leu Thr Ala Gln Ser Gln Val Gln Met Lys Lys Gln Lys Val
 580 585 590
 Ser Thr Pro Ser Asp Tyr Thr Leu Ser Phe Leu Lys Arg Gln Arg Lys
 595 600 605
 Gly Leu
 610

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..9180
- (D) OTHER INFORMATION: /note= "genomic sequence for MEN1 gene"

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1680..1766

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 1767..2264

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 2265..2732

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 2733..4296

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 4297..4505

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4506..4715

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 4716..4844

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4845..5176

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 5177..5217

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 5218..5297

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 5298..5385

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 5386..6024

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 6025..6161

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 6162..6622

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 6623..6758

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 6759..7195

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 7196..7360

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 7361..7577

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 7578..8881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGTCTTGA ACTCCTGGCC TCAAGCAATC CTCCTGCTTC AGCTTCCCAA AGTGTGTGTA	60
TTACAGGCAT GAGCCTGGCA TGAAGTTGAC ACTATTGAGA TATACTGGTC AGGTATTTTG	120
TGGAATGTCC CTCAACTCTG TTTTGCCAGA TGTTTTCTCA TGATTAGAGG AGAGTTATAA	180
ATTTTGAGGA AAATCCAGAG AGGTGAAGAG GTGAAGTAGG GCAGAAATTT AATCTGTTTT	240
ATTTACTGCT ATATACCGAG TGTCTGGAAC TTGGCCCATG GTAAGTACCA AAAATCTGTT	300
TTTTTTGAAT GAATAAGCAA ATAAATGAGT GACCGTGGAA ATTTAGTATT ATTTCAAAGT	360
TTCAAAGCGT TGTTGATACA GGCCAGGCAC AGTGGCTCAC ACCTGTAATC CCAGCACTTT	420
TGGAGGCCGA GGTAGGAGGA TCACTTGAGG TCAGGAGTTC GAGACCAGCC TGACCAACAT	480
GGTGACACCC CTGTCTCTAC TAAGTAAAT ACAAAAATTA GCCAAGTGTG GTGGCAGGCA	540

CCTGTAATCC CGGCTACTTG GGAAGCTGAG GCAGAAGAAT CACTTGAACC TGGGAGGCAG 600
 AGGTTGCAGT GAGCCGAGAT CACCCCACTG CACTCCAGCC TGAGTGACAG AGCGAGACTC 660
 TGTCTCAAAA CAAATAAACA AATAACTACT CTTTGGCCGG GTAAGGTGGT TCACGCCTGT 720
 AATTTTAGCA CTTTGGGAGG CTGAGGCGGG CAGATCACTT GAGGTTAGGG GTTCGAGACC 780
 AGTCTGGCCA ACATGGTGAA ACCCCATCTC TACTTAAAAT AAAAAAAGTT TTCTGGGTGT 840
 GGTGGCGGAC GCCTATAATC CCAGCTACTT GGGACTTTTT TTTAAGACGG AATCTCACTC 900
 TGTTGCCCAG GCTGGAGTGC AGTGGCAAGA TTCTGGCTCA CTGAAGCCTC CGCCTCCCAG 960
 GTTCAAGGGG ATTCCCCGCG CCTCAGCCTC CCAAGTAGCT GGGAATCCCT GTCTCTGCAA 1020
 AAAAAAAAAA AAAAAAAAAAC AAAAAATATA TATATATATA TATATGTGTG TGTGTGTGTG 1080
 TGTGTGTGTG TTATATGTAT ATATATTTAT GTATATGCAC ATACACACAA AATTAGGCGG 1140
 GAGTGGTGGC GCACGCCTGT GATCACAGCT ACTCGGGAGG CTGAGGCACG AGAATCGCTT 1200
 GAGCCCGTGA AGTCGAGGCT GCAGTGAGCC CAGATCGAGC CACTGCATTC CAGCCTGGGC 1260
 GAAAGAGAAA GACCGTGTCT CAAAACAAAC AAACAAAAGC TACTCTTAGC ACGTGTTAGA 1320
 GTATCTCGCG GCGGGAAGTG GGAAACGAGT GCTGCACACA GAGTAGGCAT CTTTATATGT 1380
 TAACAGACAC TGATACCCAG CTAAAGCGGC TGAACACATT TACTCTCTGG CAGTGTTTAA 1440
 AAGTATCTGT TTTTCTCATA TTGTTTTATT TTAATTTTTT CTGGATCAAG CAACCTGATC 1500
 TTTTTCCTCA TAACTTGCCG ACCGACCCGT GACAGCAAAA CCGGCAGAAG CTCGGCGACC 1560
 TCCCACCCCG AGTCTGCAGG TAGTGCCCCC GGACTIONATT TTCCAGAAGG CACTGCGGGC 1620
 ACGCTTCCTG CCTGGTCGGC CTGAAGGGAA GGGCCAATCC CTGAGTATCT CGGGAAGGAG 1680
 GTGTCCGGAG CCGCGGACCT AGAGATCCCA GAAGCCACAG CGCAGCGGCC CGGCCCCGCA 1740
 CTATTTCCAG GCTCTGCGGG GCAGGGGTGG GCCCAGACTC CACTTCCCAG CGGGTAGTGC 1800
 GACCCTAGGG GCGGGACTTC ATGTCCCAGC AGGCTCCGGG CGGCGTGCAG CGCGGTGCCT 1860
 AGTGTGGGAT GTAAGCGCGG AGGTGGGCGA GGGGGACCGA GGCCAGGACT CTCCTTGGGG 1920
 TTTGGGGGCT TGACCTGGGT GCGCTTTCTG GACAGACTTT ACAGCCCCCG GGGGCACAGT 1980
 CGTAGAGAGG GGGCGGGGCG GCCATTGGGG CTCCTCATTG GGGTGCTTGG GGCGCACCCC 2040
 ATCGGGTACC GGGCGTCCCG GAATTGTGGG GGACAAAAG GCTCTGCAGT CTCGGCTGAG 2100
 GGGTCTCACC GACAAAAGAG GGGAAGCCGG TGAGCAGAGG CTGAAGAGGG TGGGAAGCA 2160
 GGGGAGCTGT GCGTGTGTCG GGGCGGGTGG AACCTTAGCG GACCCTGGGA GGAGGCTCCC 2220
 CGGCCGAACC TGCCCGACCC TCCCTCCCCC GGCTTGCTT GCAGGCCGCC GCCACCGCC 2280
 CGCCGCCATG GGGCTGAAGG CCGCCAGAA GACGCTGTTC CCGCTGCGCT CCATCGACGA 2340
 CGTGGTGCGC CTGTTTGCTG CCGAGCTGGG CCGAGAGGAG CCGGACCTGG TGCTCCTTTC 2400

CTTGGTGCTG	GGCTTCGTGG	AGCATTCTTCT	GGCTGTCAAC	CGCGTCATCC	CTACCAACGT	2460
TCCCGAGCTC	ACCTTCCAGC	CCAGCCCCGC	CCCCGACCCG	CCTGGCGGCC	TCACCTACTT	2520
TCCCGTGGCC	GACCTGTCTA	TCATCGCCGC	CCTCTATGCC	CGCTTCACCG	CCCAGATCCG	2580
AGGCGCCGTC	GACCTGTCCC	TCTATCCTCG	AGAAGGGGGT	GTCTCCAGCC	GTGAGCTGGT	2640
GAAGAAGGTC	TCCGATGTCA	TATGGAACAG	CCTCAGCCGC	TCCTACTTCA	AGGATCGGGC	2700
CCACATCCAG	TCCCTCTTCA	GCTTCATCAC	AGGTTGGAGC	CCAGTAGGTG	GGAATCTTAT	2760
CCATGACCCA	CTTCTTCAAA	ACCCTCCATG	GTTTACAGAA	CCCTTTTAAG	AACTGTAAGC	2820
CTTGTGAGGT	TCGGCAGGTG	TTATTTTCCT	CTTTGCAGTT	GGGAAACTGA	AGCCCAGAGA	2880
GGGGAAATGA	TATGCCAAAG	TCACACACGG	CATGGCAGGG	CTGGAAGTGA	AGCCTGATCA	2940
CTTGGCTCCA	AATCATCAAC	CTCACCTCTG	CCCCCTCAGC	ACCCCCACCC	TTGCCACTGA	3000
ACAGCTACAG	GAGTTCTAAG	CATGAGACAC	AGAGGGCGGC	AGCAGATTTA	GGGGGCAAGA	3060
AGATGAAATT	GGGCTGCATT	TGAGGCAGTT	AAACAAAATA	ATGGCTATGA	AGATTTTTTTT	3120
TTTTTTTTTTT	TTTGTAGACA	GGGTCTCACT	CTGTCCCCCA	GGCTGGAGTG	CAGTGGTGTG	3180
ATCATGGCTC	ACTGCAGCCT	CAGTCTCCCT	GGGCTCAGAG	ATCCTCCAAC	CTCAGCCTCC	3240
TGAGTAGCTG	AGAGTACAGG	CATGCACCGT	GGTGCTGGTT	AATTTTTTGT	ATTTTTTTTG	3300
TAGAGATGGT	GTCTCACTAT	GTGGCCCAGA	CTGGTCTTGA	ACTCTTGGGC	TCAAGTGATC	3360
TGCCCGCCTC	AGTCTCCCAA	ATGCTGGGAT	TACAGGTGTG	AGCCACCGCA	ACTGGTGGCC	3420
TATGAAAATT	TTTTTTTTTTT	TTCAGACGGC	GTCTCACTCT	GTCGCCCAGG	CTGGAGTGCA	3480
GTGGTGCAAT	CTCGGCTCAC	TGCAAGCTCT	GCCTCCTGCT	TTCATGCCAT	TCTCCTGCCT	3540
CCTGCCTCAG	CCTCCTGAGT	AGCTGGGACT	ACAGGAGCCT	GCCACCATGC	CTGGCTAATT	3600
TTTTTTTGGA	TTTTTAGTAG	AGACGAGGTT	TCACCATGTT	AGCCAGGATG	GTCTCGATCT	3660
CCTGACCTCG	TGATCCGCCC	GCCTTGGCCT	CCCAAAGTGC	TGGGATTACA	GGCGTGAGCC	3720
ACCGCACCTG	GTCAAAAATG	TTTGAGACAG	AGAAGGGGCT	TGACCTCAAA	AGGCTTAAGA	3780
GTCAGGGCTT	GCAAAGAGCT	TTGCACCAAG	CCCGGTTGAC	TGGCAATCCC	ATCCTGGTGT	3840
GCCATATTGA	GAAGGAATCA	GAGGCTGCTT	CTCAGCTTAG	CAGGAAAAGA	GTGCAGAGAT	3900
AAATGAGGGT	TATTTGTTGG	TGGGTGTATA	GCCAGAGAGT	GTTGGCCAGC	GTCCTGT'TTT	3960
TGCCATTCCCT	GTTTAAACCT	AGTAAGTGCA	GTAAAATGGA	ATCCCTAAAT	CCATAGAATA	4020
TATAATAGAG	TTGCAGAGAA	AGACGAGGTA	GGGCCAAAGG	CTGGGTCAGC	TACAGGATAT	4080
CCAGAAAGGT	ATCTTGTTGG	ACATAGAGGG	TGTAAACAGG	GAGAGAGTCT	TTGAACACGT	4140
GGGAGGGGAA	GGATGGAGGG	ATAGTGGGCA	GGAGAATCTG	AGGTTGGGTC	ACAGGCTTGG	4200
AAAGGGAGTG	GGAGGGAGTG	TGGCCCATCA	CTACCTGGCC	CCTTTCCCCA	TGTTAAAGCA	4260

CAGAGGACCC TCTTTCATTA CCTCCCCCTT CCACAGGCAC CAAATTGGAC AGCTCCGGTG 4320
 TGGCCTTTGC TGTGGTTGGG GCCTGCCAGG CCCTGGGTCT CCGGGATGTC CACCTCGCCC 4380
 TGTCTGAGGA TCATGCCTGG GTAGTGTTTG GGCCCAATGG GGAGCAGACA GCTGAGGTCA 4440
 CCTGGCACGG CAAGGGCAAC GAGGACCGCA GGGGCCAGAC AGTCAATGCC GGTGTGGCTG 4500
 AGCGGGTATT GTTCCCTCCC CCCAGCCTTG TCCCCTTCAT ACTGTAGTAG CCCAAGCCAC 4560
 CCAAGGGACT CCATTTTCTT GGGCCACACC CCTTTCTTCC CATCACCACC CACATAGGAA 4620
 GGGGAAGACAG AAGAGCCCCT TTTCTGGCT GTCATTCCCT GAAGCAGGCA CAGGGTGGGC 4680
 CATCATGAGA CATAATGATC TCATCCCCC CTAAGAGCTG GCTGTACCTG AAAGGATCAT 4740
 ACATGCGCTG TGACCGCAAG ATGGAGGTGG CGTTCATGGT GTGTGCCATC AACCCTTCCA 4800
 TTGACCTGCA CACCGACTCG CTGGAGCTTC TGCAGCTGCA GCAGGTGAGG GCTGAGCCAA 4860
 TGGGGCAGGA CTGGGCTAGG CCAGACTTGA CTTGCTGTGG GACCCCTGGGC AGGGGCACCTT 4920
 TCCCTTCCTG AGCTTCAGCT TCCCCTCCTG GAAAAATGGG TTAGTAATTC CTGGCCTGGC 4980
 CTTTCCAGG GCTCTTGGGA GAGTAGAATT GAGATGTGAA ATTGCTTTGA CTCCATTAAA 5040
 GGGCTGGTCC CAGAATTTTG GCCCTTCCAC ATGGTGGGTG GTCCCTGTTG GTTCTGACCC 5100
 CCACCTCTGC CCGATAGGCT AAGGACCCGT TCTCCTCCCT GTTCCGTGGC TCATAACTCT 5160
 CTCCTTCGGC TCCTAGAAGC TGCTCTGGCT GCTCTATGAC CTGGGACATC TGGAAAGGTC 5220
 AGTAGAGGGA AGTGGCCAGG CTGCGCCTGG TGAGGCCGGG GGGCTGGGTG GCAGCCTGAA 5280
 TTATGATCCT TTCCTAGGTA CCCCATGGCC TTAGGGAACC TGGCAGATCT AGAGGAGCTG 5340
 GAGCCCACCC CTGGCCGGCC AGACCCACTC ACCCTCTACC ACAAGGTGGG GGCATCTAAG 5400
 GAGGGTGACG AAGGGAGACC CTAACAGTGG CTGAGGCAGG GGCCCTCATC TGGGCAGATG 5460
 AGAAGAGAAC TTTGTGTGTT GGGGGGTATC GCCCATCCAG TCTCACTTTG TGTCAACTGT 5520
 GTGCAGAATC AGTTCAGTCA GGGCTGTCTG AGGGGTGTCC AGGGTTCCCC AGCCTGGGAG 5580
 TGGCAGGGGC TGCATTTGTC CCCTCAGCCC TGCCTTTTCT GCCACTGCTT ACTGTCCTTC 5640
 CTGGAGTATA ACAGAGGTCA AATGTGGTAG GAGCACTGAA GAGGGGGTGT TCACTTGGTG 5700
 GGTGTAGGTG GGGAGGAGGG CCATTGGGCT GGGCTTGAAA GTCTTTGGTG ATGTGTAGAA 5760
 GAGTGTCTGA GAAAGAGAAG GGCCCTGAGC TCGGAGGGCA GGCCCCACCC CTGCAGTCTG 5820
 CCCCAGGCCT CAGCCAGCAG TCCTGTAGAC CCAGGGAGGA GACCAGGTAG AAGGGCTGGC 5880
 AGCGAGTGGA GGTGGGAGTG GAGATGGAGA GGA CTCCCTG GGATCTTCCT GTGGCCCCTT 5940
 CTGGGTGTGC CCTGGTGGGG CATTTGTGCC AGCAGGGCAG CTGGGGCTGC CTCCCTGAGG 6000
 ATCCTCTGCC TCACCTCCAT CCAGGGCATT GCCTCAGCCA AGACCTACTA TCGGGATGAA 6060
 CACATCTACC CCTACATGTA CCTGGCTGGC TACCACTGTC GCAACCGCAA TGTGCGGGAA 6120

GCCCTGCAGG CCTGGGCGGA CACGGCCACT GTCATCCAGG AGTGAGGATC CCCCTACTAG 6180
 GGCCTGCAGC CTGTCCTTTC TTCCCCTCCA TCAGTTTCCA ACCACCCCTCG TCCAGGACTG 6240
 AGGCCTGGCT CCCACGCCCC ATCCCCTTTC CATCCAGTCC CTAGGCAGCA AGGCCACCAT 6300
 TACCCAGGAG GTAGGGACCC TGATTAAGGT GTCACATCTT TCCCTCCCTC CCCTCTCCTC 6360
 CTAATTTTTT TTTTCTCAGA ACAGTCTCAA ATCTCCAATG TTTAACCACC ATCATCCAGC 6420
 AGTGGGACTT CCACCCTCGG CCCCATGCCC CCCTCCTCAT TCTTGCTTTC TTCCTCTGGG 6480
 CTGACCCAGA CAGCATCATT TTGCAGTGAG GACCCACCT ACTCCCCCAG CCCCTGGGGG 6540
 CTCCATCCCC CGCCAGGTCC CTGGGGCTAC CCCCGATGGT GAGACCCCTT CAGACCCTAC 6600
 AGAGACCCCA CTGCTCTCAC AGCTACAAC ACTGCCGGGA AGACGAGGAG ATCTACAAGG 6660
 AGTTCTTTGA AGTAGCCAAT GATGTCATCC CCAACCTGCT GAAGGAGGCA GCCAGCTTGC 6720
 TGGAGGCGGG CGAGGAGCGG CCGGGGGAGC AAAGCCAGGT GAAAGGCTGG AGCTCCAGCC 6780
 TG TG TCCAGC CTCCCACCTG GACAGGGCTC CCTTCCACAG GGCCATGGGG GCTGCATGTA 6840
 CGGGATTAGG GATGGCAGGA GGAAGGTGGC CCTGAGCAGA CAGCTATGTT CCCTTTTGCT 6900
 ATAACTGAGG TCCTGGGCCC ACGTTGGACG GGAAGTGAAG TATTTTAGAG GTTCTACCC 6960
 TGTGCCTTCA GTTTCATGGC CAGACTCCCT CCCTCAGCTG AGGGGTGGAG GTAGGGATGG 7020
 TACGTCCTGG CTATGGATTG GCTTTATAAA AGGAAAGAGG TTCTAAGAAT GTTCCCAACC 7080
 TATGCTTACC TTTTCTGGAG CCAGGGGTCT TTGCCTAGGT GGGGGGCCTG GCCTGTGCCC 7140
 TCTGCTAAGG GGTGAGTAAG AGACTGATCT GTGCCCTCCC TTCCCCCTCG TCCAGGGCAC 7200
 CCAGAGCCAA GGTTCCGCCC TCCAGGACCC TGAGTGCTTC GCCCACCTGC TGCGATTCTA 7260
 CGACGGCATC TGCAAATGGG AGGAGGGCAG TCCCACGCCT GTGCTGCACG TGGGCTGGGC 7320
 CACCTTTCTT GTGCAGTCCC TAGGCCGTTT TGAGGGACAG GTGAGGGACA GCTGCACAGA 7380
 GGTCTGGGCA CTACAGGTGG TGACAGCAGC CACGGGCTTG TCAGACTTTT CTGGCCCAGG 7440
 GGCAGCATCT GCCCATCCCC TTCGGTGCCG ATGGGACTGA GACCCCTGG GTGGGATGGG 7500
 ATGGCCAGAG CAGGGTCCTG GAGTTCAGC CACTGGCCGG CAACCTTGCT CTCACCTTGC 7560
 TCTCCCCACT GGCCAGGTG CGGCAGAAGG TGCGCATAGT GAGCCGAGAG GCCGAGGCGG 7620
 CCGAGGCCGA GGAGCCGTGG GGCGAGGAAG CCCGGAAGG CCGGCGGCGG GGCCACGGC 7680
 GGGAGTCCAA GCCAGAGGAG CCCCCGCCG CCAAGAAGCC AGCACTGGAC AAGGGCCTGG 7740
 GCACCGGCCA GGGTGCAAGT TCAGGACCCC CCCGGAAGCC TCCTGGGACT GTCGCTGGCA 7800
 CAGCCCGAGG CCCTGAAGGT GGCAGCACGG CTCAGGTGCC AGCACCCGCA GCATCACCAC 7860
 CGCCGGAGGG TCCAGTGCTC ACTTTCCAGA GTGAGAAGAT GAAGGGCATG AAGGAGCTGC 7920
 TGGTGGCCAC CAAGATCAAC TCGAGCGCCA TCAAGCTGCA ACTCACGGCA CAGTCGCAAG 7980

TGCAGATGAA GAAGCAGAAA GTGTCCACCC CTAGTGACTA CACTCTGTCT TTCCTCAAGC 8040
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 CGCCTTAGTC CCCCAACTCT GAGCCCATGT TCTGCCCCCA GCCCAAAGGG GACAGGCCTC 8160
 ACCTCTACCC AAACCCTAGG TTCCCGGTCC CGAGTACAGT CTGTATCAAA CCCACGATTT 8220
 TCTCCAGCTC AGAACCCAGG GCTCTGCCCC AGTCGTTAGA ATATAGGTCT CTTCTCCCAG 8280
 AATCCCAGCC GGCCAATGGA AACCTCACGC TGGGTCCTAA TTACCAGTCT TTAAAGGCCC 8340
 AGCCCCTAGA AACCCAAGCT CCTCCTCGGA ACCGCTCACC TAGAGCCAGA CCAACGTTAC 8400
 TCAGGGCTCC TCCAGCTTG TAGGAGCTGA GGTTCACCC TTAACCCAAG GGAGCACAGG 8460
 TCCCACCTCC AGCCCGGGGA GCCTAGGACC ACTCAGCCCC TAGGAGTATA TTTCCGCACT 8520
 TCAGAATTCC ATATCTTGCG AATCCAAGCT CCCTGCCCCA AATAACTTCA GTCCTGCTTC 8580
 CAGAATTTGG AAATCCTAGT TTCCTCTCCT TCGTATCCCG AGTCTGGGAC ACAAACCTCC 8640
 GCCCCCAGCC TATGAGCATC CTGAGCCCCG CCCTCTTCCT GACGAAACTG GCCCCGGATC 8700
 AGAGCAGGAC CTCCCTTCCG ACCCTCTGGG AACCTCCCAG AGGTCCAGCC CATCTCGGAG 8760
 CATCCCGGAG GAAATCTGCA GAGGGGTTAG GAGTGGGTGA CAAGAGCCTG ATCTCTTCCT 8820
 GTTTTGTACA TAGATTTATT TTTCAGTTCC AAGAAAGATG AATACATTTT GTTAAAAAAA 8880
 ATATAAAGCG CAAGTCCATG TTTATCTGGG AAATTGGGGA TGGGGCGGGG AGTGGAGCGC 8940
 CCCTTCTTCC CTTTGTCTTC TGGCTCCCGG GACTTTGCGC TCCCTACCTG TGGAGCGCGA 9000
 GCGACAGTGG CGGCGGAAGG ACGTAGGCTC CGCCCCGGCC TTGGGGCTTC CCCC GCGCCG 9060
 CCGAGGGCCC GTCCCGCGGG CGCCTCCTCC CGGACTGGCG GTGGGGCATC CCNNGGCGCG 9120
 GCCCCGCCCC CGGGCTTCAG CCCC GCCCCC GCGGCTTCAG AGCCACGGGC GCCCGCCCCG 9180

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "antisense strand from patient with 512delC frameshift mutation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCTTAAG TAGGAGCGG

19

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from normal sequence (positions 500-519 of MEN1 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCTTGAA GTAGGAGCGG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from normal sequence (positions 1405-1424 of MEN1 cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCCCAG CCCACGTGCA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from position 1417 C->T substitution, resulting in W436X mutation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTGGCCTAG CCCACGTGCA

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACCTGGGTG CGCTTTCTGG AC

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTGGACATA GAGGGTGTAACACAG

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGAGCTCG GGAACGTTGG TAG

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGACCTTCT TCACCAGCTC ACGG

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAACCTCAC AAGGCTTACA GTTC

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTTGGACATA GAGGGTGTAACACAG

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACAGTTGACA CAAAGTGAGA CTGG

24

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCTTCTG TCTTCCTTC CTATG

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCCCACAG CAAGTCAAGT CTGG

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTGTTCCGT GGCTCATAAC TCTC

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTCAGCCAG CAGTCCTGTA GA

22

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGACGAGGGT GGTGGAAC TG

22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGACTCCTTG GGATCTTCCT GTG

23

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AACGACCATC ATCCAGCAGT GG

22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCATCCCTAA TCCCGTACAT GC

22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGTGAGACC CCTTCAGACC CTAC

24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGCTAAGGG GTGAGTAAGA GAC

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTTTGATAC AGACTGTACT CGG

23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCTGACAAG CCCGTGGCTG CTG

23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCATCTGCCC ATCCCCTTCG GTG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAAGCCTCCT GGGACTGTCG CTG

23

Conc